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COMPOUNDS FOR TREATMENT OF INFECTIOUS AND IMMUNE SYSTEM DISORDERS AND METHODS FOR THEIR USE

Reference to Related Applications

This application is a continuation-in-part of U.S. Patent Application No. 10/100,679, filed March 14, 2002; which is a continuation-in-part of U.S. Patent Application No. 09/450,072, filed November 29, 1999, now U.S. Patent 6,358,734; which is a continuation-in-part of U.S. Patent Application No. 09/351,348, filed July 12, 1999, now U.S. Patent 6,436,898, and claims priority to PCT International Patent Application PCT/NZ00/00121 filed on July 10, 2000.

Technical Field

The present invention relates generally to the detection, treatment and prevention of infectious diseases. In particular, the invention is related to compounds comprising immunogenic epitopes isolated from *Mycobacterium vaccae*, and the use of such compounds in vaccination or immunotherapy against infectious disease, including mycobacterial infections such as infection with *Mycobacterium tuberculosis* or *Mycobacterium avium,* and in certain treatments for immune disorders and cancer.

Background of the Invention

The present invention relates generally to the treatment and prevention of infectious diseases, and to the treatment of certain immune disorders and cancers. In particular, the invention is related to compounds and methods for the treatment and prevention of mycobacterial infections, including infection with *Mycobacterium tuberculosis* or *Mycobacterium avium*.

Tuberculosis is a chronic, infectious disease that is caused by infection with *Mycobacterium tuberculosis* (*M. tuberculosis*). It is a major disease in developing countries, as well as an increasing problem in developed areas of the world, with about 8 million new cases

and 3 million deaths each year. Although the infection may be asymptomatic for a considerable period of time, the disease is most commonly manifested as a chronic inflammation of the lungs, resulting in fever and respiratory symptoms. If left untreated, significant morbidity and death may result.

Although tuberculosis can generally be controlled using extended antibiotic therapy, such treatment is not sufficient to prevent the spread of the disease. Infected individuals may be asymptomatic, but contagious, for some time. In addition, although compliance with the treatment regimen is critical, patient behavior is difficult to monitor. Some patients do not complete the course of treatment, which can lead to ineffective treatment and the development of drug resistant mycobacteria.

Inhibiting the spread of tuberculosis requires effective vaccination and accurate, early diagnosis of the disease. Currently, vaccination with live bacteria is the most efficient method for inducing protective immunity. The most common mycobacterium employed for this purpose is Bacillus Calmette-Guerin (BCG), an avirulent strain of *Mycobacterium bovis*. However, the safety and efficacy of BCG is a source of controversy and some countries, such as the United States of America, do not vaccinate the general public. Diagnosis of *M. tuberculosis* infection is commonly achieved using a skin test, which involves intradermal exposure to tuberculin PPD (protein-purified derivative). Antigen-specific T cell responses result in measurable induration at the injection site by 48-72 hours after injection, thereby indicating exposure to mycobacterial antigens. Sensitivity and specificity have, however, been a problem with this test, and individuals vaccinated with BCG cannot be distinguished from infected individuals.

A less well-known mycobacterium that has been used for immunotherapy for tuberculosis, and also leprosy, is *Mycobacterium vaccae*, which is non-pathogenic in humans. However, there is less information on the efficacy of *M. vaccae* compared with BCG, and it has not been used widely to vaccinate the general public. *M. bovis* BCG and *M. vaccae* are believed to contain antigenic compounds that are recognized by the immune system of individuals exposed to infection with *M. tuberculosis*.

Several patents and other publications disclose treatment of various conditions by administering mycobacteria, including *M. vaccae*, or certain mycobacterial fractions. International Patent Publication WO 91/02542 discloses treatment of chronic inflammatory

disorders in which a patient demonstrates an abnormally high release of IL-6 and/or TNF or in which the patient's IgG shows an abnormally high proportion of agalactosyl IgG. Among the disorders mentioned in this publication are psoriasis, rheumatoid arthritis, mycobacterial disease, Crohn's disease, primary biliary cirrhosis, sarcoidosis, ulcerative colitis, systemic lupus erythematosus, multiple sclerosis, Guillain-Barre syndrome, primary diabetes mellitus, and some aspects of graft rejection. The therapeutic agent preferably comprises autoclaved *M. vaccae* administered by injection in a single dose.

U.S. Patent 4,716,038 discloses diagnosis of, vaccination against and treatment of autoimmune diseases of various types, including arthritic diseases, by administering mycobacteria, including *M. vaccae.* U.S. Patent 4,724,144 discloses an immunotherapeutic agent comprising antigenic material derived from *M. vaccae* for treatment of mycobacterial diseases, especially tuberculosis and leprosy, and as an adjuvant to chemotherapy. International Patent Publication WO 91/01751 discloses the use of antigenic and/or immunoregulatory material from *M. vaccae* as an immunoprophylactic to delay and/or prevent the onset of AIDS. International Patent Publication WO 94/06466 discloses the use of antigenic and/or immunoregulatory material derived from *M. vaccae* for therapy of HIV infection, with or without AIDS and with or without associated tuberculosis.

Traditional vaccines contain the disease-causing organism (or a component thereof) in either attenuated or killed form. As an alternative approach to traditional vaccines, DNA vaccines have been developed for diseases as diverse as AIDS, influenza, cancer and malaria. Clinical trials of DNA vaccines are in progress for a number of these diseases. A typical DNA vaccine consists of DNA encoding an antigen cloned in a non-active plasmid carrier. Expression of the antigen encoded by the vaccine DNA is usually under control of a strong promoter, such as human β-actin, Rous sarcoma virus (RSV) or CMV promoter (Ramsay AJ, *et al. Immunology and Cell Biology* 75:360-363, 1997). The first experimental evidence that DNA vaccines were able to induce the desired immune response was produced by Tang *et al.* (Tang D-C, *et al. Nature* 356:152-154, 1992). In these experiments, mice inoculated with plasmids containing the gene encoding for human growth hormone developed specific primary antibody responses.

Immune responses to two DNA vaccines containing genes from *M. tuberculosis* have been evaluated in animal models. The first vaccine contained the gene coding for the GroEL

stress protein (65 kDa protein; Tascon RE, *et al. Nature Med.* 2:888-892, 1996). Mice injected with this DNA vaccine were protected at a level equivalent to mice receiving the traditional BCG vaccine. The second DNA vaccine against *M. tuberculosis* contained DNA encoding an antigen from the antigen 85 complex and similar results to the study by Tang *et al.* were obtained (Huygen K, *et al. Nature Med.* 2:893-898, 1996). U.S. Patent 5,736,524 discloses vaccination of domestic mammals or livestock against infection by *M. tuberculosis* or *M. bovis* by administering a polynucleotide vaccine comprising the *M. tuberculosis* antigen 85 gene operably linked to transcription regulatory elements.

The first human DNA vaccine trial was reported by Wang *et al.* (Wang R, *et al. Science* 282:476-80, 1998). In this trial, an antigen from *Plasmodium falciparum*, the causative agent of malaria, was injected into healthy volunteers. The desired immune response was elicited, as demonstrated by the presence of cytotoxic T ($CD8^+$) lymphocytes (CTL), suggesting that the immune system would be able to clear parasites from infected patients. Safety and immunogenicity of a human DNA vaccine against HIV-1 infection was determined in a trial performed by McGregor *et al.* (*J. Infect. Dis.* 178:92-100, 1998). Experimental data from other DNA vaccine experiments has also suggested that antibodies, MHC class 1-restricted $CD8^+$ CTL and class II-restricted $CD4^+$ helper T cells are produced following injection with DNA vaccines (Ramsay, AJ *et al. Immunology and Cell Biology* 75:360-363, 1997).

DNA vaccines have distinct advantages over more traditional vaccines containing killed or attenuated organisms. DNA vaccination induces immune responses that are long-lived and therefore only a single inoculation may be required. DNA encoding a number of antigens may be incorporated into a single plasmid thereby providing protection against a number of diseases. The technology for DNA vaccine production is relatively simple and the same technology can be used to produce all vaccines, with a resulting cheaper production cost. Delivery of efficacious traditional vaccines to the patient are dependent on maintaining an unbroken "cold chain" from manufacturer to clinic. DNA vaccines produced in solution or in dried form are not sensitive to storage conditions.

More recently, alternative ways of constructing and applying DNA vaccines have been developed. In one of the techniques, called Somatic Transgene Immunization (STI), the plasmid DNA carrying an immunoglobulin heavy chain gene under the control of tissue-specific

regulatory elements was inoculated directly into the spleen of mice, with subsequent expression of the antigen on the surface of B-cells (Xiong S, *et al. Proc. Natl. Acad. Sci. USA* 94:6352-6357, 1997). These B cells produced antibodies against the expressed antigen, leading to an immune response. Subsequent studies showed that STI induced persistent immunologic memory for up to two years (Gerloni M, *et al. Vaccine* (2-3):293-297, 1998).

Expression Library Immunization (ELI) is another technique employing DNA vaccines (Barry MA, *et al. Nature* 377:632-635, 1995). In this technique, fragments of the complete genome of a pathogen are cloned into a vector and used as vaccine. Selection of protective antigen(s), particularly those inducing CTL, is done by screening and re-screening pools of clones until single clones can be identified. The polynucleotide or polypeptide identified may then be incorporated into a proven delivery system.

Progress on the development of an epitope-based vaccine for the treatment and prevention of HIV infection by scientists at Epimmune Inc. (San Diego, CA), has recently been published (Ishioka GY, *et al., Journal of Immunology* 162:3915-3925, 1999).

There remains a need in the art for effective compounds and methods for preventing and treating infectious disorders, such as tuberculosis and other mycobacterial infections in humans and in domestic mammals or livestock, and for the treatment of certain immune system-related disorders.

Summary of the Invention

Briefly stated, the present invention provides compounds and methods for the prevention and treatment of infectious diseases, such as mycobacterial infections, and for the enhancement of immune responses, such as in the treatment of immune disorders and cancers.

In a first aspect, isolated polynucleotides are provided that are derived from the *M. vaccae* genome. These polynucleotides encode polypeptide epitopes selected on the basis of their immunogenic properties as illustrated by results from a number of immunological assays. In specific embodiments, the inventive polynucleotides comprise a sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 8-21; (b) sequences having at least 75%, 90% or 95% identity to a sequence of SEQ ID NO: 8-21, determined as described below; and (c) complements of the sequences of (a) and (b).

In a second aspect, the invention provides isolated polypeptides comprising an immunogenic epitope of a *M. vaccae* antigen. In specific embodiments, the inventive polypeptides comprise a sequence selected from the group consisting of: (a) sequences provided in SEQ ID NO: 64-77; and (b) sequences having at least 75%, 90% or 95% identity to a sequence of SEQ ID NO: 64-77, determined as described below.

Genetic constructs comprising at least one of the inventive polynucleotides, and host cells transformed or transfected with such genetic constructs are also provided.

In another aspect, the present invention provides fusion proteins comprising at least one polypeptide of the present invention. In specific embodiments, such fusion proteins comprise a sequence of SEQ ID NO: 79-81, 90-97 or 116. Polynucleotides encoding such fusion proteins are also provided. In certain embodiments, such polynucleotides comprise a sequence of SEQ ID NO: 56-58, 82-89 or 115.

Within other aspects, the present invention provides compositions that comprise at least one of the inventive polypeptides, polynucleotides, fusion proteins or genetic constructs, and a physiologically acceptable carrier. The invention also provides compositions comprising at least one of the above polypeptides, polynucleotides, fusion proteins or genetic constructs and an immunostimulant.

In yet another aspect, methods are provided for enhancing an immune response in a patient, comprising administering to a patient an effective amount of one or more of the above compositions. In one embodiment, the immune response is a Th1 response.

In further aspects of this invention, methods are provided for the treatment of a disorder in a patient, comprising administering to the patient a composition of the present invention. In certain embodiments, the disorder is selected from the group consisting of immune disorders, infectious diseases and cancer.

These and other aspects of the present invention will become apparent upon reference to the following detailed description. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

Brief Description of the Drawings

Figs. 1A-F illustrate the induction of protective immunity, measured as a decrease in *M. tuberculosis* CFU in lung and spleen homogenates of BALB/cByJ mice, by vaccination with *M. bovis* BCG (Figs. 1A and D, respectively), with ME/D DNA (Figs. 1B and E, respectively), or with rME/D (Fig. 1C and F, respectively).

Figs. 2A-D show the proliferative responses of lymph node cells from BALB/cByJ mice immunized subcutaneously with rME/A (Fig. 2A), rME/B (Fig. 2B) or rME/D (Fig. 2C). Control mice were immunized with PBS (Fig. 2D).

Figs. 3A-D illustrate IFN-γ secretion by lymph node cells from BALB/cByJ mice immunized subcutaneously with recombinant multi-epitope constructs rME/A (Fig. 3A), rME/B (Fig. 3B) or rME/D (Fig. 3C). Control mice were immunized with PBS (Fig. 3D).

Fig. 4A demonstrates the proliferative responses of lymph node cells from BALB/cByJ mice immunized with rME/A, rME/D or ME/D DNA by three different routes of immunization. The proliferative response of lymph node cells from control mice immunized with PBS is shown in Fig. 4B.

Fig. 5A demonstrates the level of IFN-γ secretion by lymph node cells from BALB/cByJ mice immunized with rME/A, rME/D or ME/D DNA by three different routes of immunization. The level of IFN-γ secretion by control mice immunized with PBS is shown in Fig. 5B.

Fig. 6A shows the contribution of single epitopes to the proliferative responses of lymph node cells from BALB/cByJ mice immunized with rME/A, rME/D or ME/D DNA by three different routes of immunization. The proliferative response of lymph node cells from control mice immunized with PBS is shown in Fig. 6B.

Fig. 7A demonstrates the contribution of single epitopes to the level of IFN-γ secretion by lymph node cells from BALB/cByJ mice immunized with rME/A, rME/D or ME/D DNA by three different routes of immunization. The level of IFN-γ secretion by control mice immunized with PBS is shown in Fig. 7B.

Figs. 8A and B illustrate the titer and subclass of anti-ME antibodies in the serum of mice immunized with ME/D DNA that reacted with rME/A and rME/D *in vitro*. The titres of IgG1 antibodies are shown in Fig. 8A, with the titer of IgG2a antibodies being shown in Fig. 8B.

Figs. 9A-C show the IFN-γ secretion by memory splenocytes from BALB/cByJ mice immunized with recombinant single epitopes (Fig. 9B) or rME/D (Fig. 9C). IFN-γ secretion by splenocytes after stimulation with controls is shown in Fig. 9A.

Figs. 10A and B demonstrate the IFN-γ secretion (Fig. 10A) and proliferative response (Fig. 10B) by human PBMC after stimulation *in vitro* with rME/A, rME/B or rME/D.

Figs. 11A and B demonstrate the IFN-γ secretion (Fig. 11A) and proliferative response (Fig. 11B) by human PBMC after stimulation *in vitro* with eight recombinant single epitopes.

Detailed Description of the Invention

As noted above, the present invention is generally directed to compositions and methods for preventing and treating disorders, including infectious diseases, and for stimulating an immune response in a patient, such as, for example, in the treatment of certain immune disorders and cancers. Examples of such disorders which may be effectively treated employing the inventive methods and compositions include, but are not limited to, mycobacterial infections, including *M. tuberculosis* and *M. avium* infections, and disorders in which the stimulation of a Th1 immune response is beneficial, including (but not limited to) psoriasis and allergic rhinitis.

Certain pathogens, such as *M. tuberculosis*, as well as certain cancers, are effectively contained by an immune attack directed by $CD4^+$ T cells, known as cell-mediated immunity. Other pathogens, such as poliovirus, also require antibodies, produced by B cells, for containment. These different classes of immune attack (T cell or B cell) are controlled by different subpopulations of $CD4^+$ T cells, commonly referred to as Th1 and Th2 cells.

The two types of Th cell subsets have been well characterized in a murine model and are defined by the cytokines they release upon activation. The Th1 subset secretes IL-2, IFN-γ and tumor necrosis factor, and mediates macrophage activation and delayed-type hypersensitivity response. The Th2 subset releases IL-4, IL-5, IL-6 and IL-10, which stimulate B cell activation. The Th1 and Th2 subsets are mutually inhibiting, so that IL-4 inhibits Th1-type responses, and IFN-γ inhibits Th2-type responses. Similar Th1 and Th2 subsets have been found in humans, with release of the identical cytokines observed in the murine model. Amplification of Th1-type immune responses is central to a reversal of disease state in many disorders, including

disorders of the respiratory system such as tuberculosis, sarcoidosis, asthma, allergic rhinitis and lung cancers.

In one aspect, the compositions of the present invention include polypeptides that comprise at least one immunogenic epitope of a *M. vaccae* antigen, or a variant thereof. In specific embodiments, the inventive polypeptides comprise a sequence provided in SEQ ID NO: 61-77. Such polypeptides stimulate T cell proliferation, and/or interferon gamma secretion from T cells of individuals exposed to *M. tuberculosis*.

As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full-length proteins (*i.e.*, antigens), wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising an immunogenic epitope of one of the above antigens may consist entirely of the immunogenic epitope, or may contain additional sequences. The additional sequences may be derived from the native *M. vaccae* antigen or may be heterologous, and such sequences may (but need not) be immunogenic.

"Immunogenic," as used herein, refers to the ability to elicit an immune response in a patient, such as a human, or in a biological sample. In particular, an immunogenic epitope is that portion of a polypeptide that is capable of stimulating cell proliferation, interleukin-12 production or interferon-γ production in biological samples comprising one or more cells selected from the group of T cells, NK cells, B cells and macrophages, where the cells are derived from a mycobacteria-immune individual. In general, an immunogenic epitope will stimulate proliferation of PBMC from mycobacteria-immune individuals at levels at least two-fold greater than that observed in control PBMC, determined using assay techniques detailed below in Example 1. Alternatively, or additionally, an immunogenic epitope will stimulate the production of interferon-γ in PBMC from mycobacteria-immune individuals at levels that are at least two-fold greater than those observed in control cells as determined by at least a two-fold increase in OD in an ELISA assay as detailed in Example 1. A mycobacteria-immune individual is one who is considered to be resistant to the development of mycobacterial infection by virtue of having mounted an effective T cell response to *M. tuberculosis,* to environmental saprophytes, or to BCG. Such individuals may be identified based on a strongly positive (*i.e.*, greater than about 10 mm diameter induration) intradermal skin test response to tuberculosis proteins (PPD), and an absence of any symptoms of tuberculosis infection. Polypeptides comprising at least an

immunogenic epitope of one or more *M. vaccae* antigens may generally be used to induce protective immunity against tuberculosis in a patient and/or to stimulate an immune response in a patient.

In another aspect, the compositions of the present invention comprise isolated polynucleotides that encode polypeptides and/or fusion proteins comprising an immunogenic epitope of a *M. vaccae* antigen. In specific embodiments, the inventive polynucleotides comprise a sequence of SEQ ID NO: 8-21, 56-58, 82-89 or 115. Complements of the inventive isolated polynucleotides, reverse complements of such isolated polynucleotides and reverse sequences of such isolated polynucleotides are also provided, together with variants of such sequences. The present invention also encompasses polynucleotide sequences that differ from the disclosed sequences but which, due to the degeneracy of the genetic code, encode a polypeptide which is the same as that encoded by a polynucleotide sequence disclosed herein.

The term "polynucleotide(s)," as used herein, means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and corresponding RNA molecules, including HnRNA and mRNA molecules, both sense and anti-sense strands, and comprehends cDNA, genomic DNA and recombinant DNA, as well as wholly or partially synthesized polynucleotides. An HnRNA molecule contains introns and corresponds to a DNA molecule in a generally one-to-one manner. An mRNA molecule corresponds to an HnRNA and/or DNA molecule from which the introns have been excised. A polynucleotide may consist of an entire gene, or any portion thereof. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all such operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well known in the art and are described, for example, in Robinson-Benion *et al.* "Antisense techniques," *Methods in Enzymol.* 254:363-375, 1995; and Kawasaki *et al. Artific. Organs* 20:836-848, 1996.

The definition of the terms "complement", "reverse complement" and "reverse sequence", as used herein, is best illustrated by the following example. For the sequence 5' AGGACC 3', the complement, reverse complement and reverse sequence are as follows:

complement	3' TCCTGG 5'
reverse complement	3' GGTCCT 5'

reverse sequence 5' CCAGGA 3'.

Preferably, sequences that are complements of a specifically recited polynucleotide sequence are complementary over the entire length of the specific polynucleotide sequence.

All the polynucleotides and polypeptides provided by the present invention are isolated and purified, as those terms are commonly used in the art. Preferably, the inventive polypeptides and polynucleotides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure.

The compositions and methods of this invention also encompass variants of the above polypeptides and polynucleotides. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 75%, more preferably at least 80%, more preferably at least 90%, more preferably yet at least 95%, and most preferably at least 98% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100. By way of example only, assume a queried polynucleotide having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the alignment produced by the BLASTN algorithm using the default parameters as described below. The 23 nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage identity of the queried polynucleotide to the hit in the EMBL database is thus 21/220 times 100, or 9.5%. The percentage identity of polypeptide sequences may be determined in a similar fashion.

Polynucleotide and polypeptide sequences may be aligned, and percentages of identical residues in a specified region may be determined against another polynucleotide or polypeptide sequence, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA

algorithms. Polynucleotides may also be analyzed using the BLASTX algorithm, which compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database. The percentage identity of polypeptide sequences may be examined using the BLASTP algorithm. The BLASTN, BLASTP and BLASTX algorithms are available on the NCBI anonymous FTP server and from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894, USA. The BLASTN algorithm Version 2.0.11 [Jan-20-2000], set to the parameters described below, is preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm, set to the parameters described below, is preferred for use in the determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX, is described in the publication of Altschul, *et al.*, *Nucleic Acids Res.* 25: 3389-3402, 1997.

The FASTA and FASTX algorithms are available on the Internet, and from the University of Virginia by contacting the Vice Provost for Research, University of Virginia, P.O. Box 9025, Charlottesville, VA 22906-9025, USA. The FASTA algorithm, set to the default parameters described in the documentation and distributed with the algorithm, may be used in the determination of polynucleotide variants. The readme files for FASTA and FASTX Version 1.0x that are distributed with the algorithms describe the use of the algorithms and describe the default parameters. The use of the FASTA and FASTX algorithms is described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and Pearson, *Methods in Enzymol.* 183:63-98, 1990.

The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the E values and percentage identity for polynucleotides: Unix running command with the following default parameters: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq –o results; and parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (blastn only) [Integer]; -v Number of one-

line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File Out] Optional.

The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the E values and percentage identity of polypeptide sequences: blastall –p blastp –d swissprotdb –e 10 -G 0 -E 0 –v 30 –b 30 –i queryseq –o results; the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

The "hits" to one or more database sequences by a queried sequence produced by BLASTN, BLASTP, FASTA, or a similar algorithm, align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence. The BLASTN, FASTA and BLASTP algorithms also produce "Expect" values for polynucleotide and polypeptide alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being related. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN algorithm. E values for polypeptide sequences may be determined in a similar fashion using various polypeptide databases, such as the SwissProt database.

According to one embodiment, "variant" polynucleotides and polypeptides, with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleic or amino acids than each of the

polynucleotides or polypeptides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% probability of being the same as the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN, FASTA or BLASTP algorithms set at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being the same as the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN algorithm set at the default parameters. Similarly, according to a preferred embodiment, a variant polypeptide is a sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99% probability of being the same as the polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP algorithm set at the default parameters.

In addition to having a specified percentage identity to an inventive polynucleotide or polypeptide sequence, variant polynucleotides and polypeptides preferably have additional structure and/or functional features in common with the inventive polynucleotide or polypeptide. Polypeptides having a specified degree of identity to a polypeptide of the present invention share a high degree of similarity in their primary structure and have substantially similar functional properties. In addition to sharing a high degree of similarity in their primary structure to polynucleotides of the present invention, polynucleotides having a specified degree of identity to, or capable of hybridizing to, an inventive polynucleotide preferably have at least one of the following features: (i) they contain an open reading frame or partial open reading frame encoding a polypeptide having substantially the same functional properties as the polypeptide encoded by the inventive polynucleotide; or (ii) they contain identifiable domains in common.

In certain embodiments, variant polynucleotides hybridize to a polynucleotide of the present invention under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65°C.

The present invention also encompasses polynucleotides that differ from the disclosed sequences but that, as a consequence of the discrepancy of the genetic code, encode a polypeptide having similar functional activity as a polypeptide encoded by a polynucleotide of the present invention. Thus, polynucleotides comprising sequences that differ from the polynucleotide sequences disclosed herein (or complements, reverse sequences, or reverse complements of those sequences) as a result of conservative substitutions are encompassed within the present invention. Additionally, polynucleotides comprising sequences that differ from the inventive polynucleotide sequences or complements, reverse complements, or reverse sequences as a result of deletions and/or insertions totaling less than 10% of the total sequence length are also contemplated by and encompassed within the present invention. Similarly, polypeptides comprising sequences that differ from the inventive polypeptide sequences as a result of amino acid substitutions, insertions, and/or deletions totaling less than 10% of the total sequence length are contemplated by and encompassed within the present invention, provided the variant polypeptide has similar activity to the inventive polypeptide.

A polypeptide of the present invention may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

As used herein, the term "*x*-mer," with reference to a specific value of "*x*," refers to a polynucleotide comprising at least a specified number ("*x*") of contiguous residues of any of the polynucleotides identified as SEQ ID NO: 8-21, 56-58, 82-89 and 115. The value of *x* may be from about 20 to about 600, depending upon the specific sequence.

Polynucleotides of the present invention comprehend polynucleotides comprising at least a specified number of contiguous residues (*x*-mers) of any of the polynucleotides identified as SEQ ID NO: 8-21, 56-58, 82-89 and 115 or their variants. According to preferred embodiments, the value of *x* is preferably at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a

150-mer, a 180-mer, a 220-mer a 250-mer, or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide identified as SEQ ID NO: 8-21, 56-58, 82-89 or 115 or a variant of one of the polynucleotides identified as SEQ ID NO: 8-21, 56-58, 82-89 or 115.

In general, the inventive polypeptides and polynucleotides, may be prepared using any of a variety of procedures. For example, polypeptides may be produced recombinantly by inserting a polynucleotide that encodes the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a polynucleotide that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, mycobacteria, insect, yeast or a mammalian cell line such as COS or CHO. The polynucleotides expressed in this manner may encode naturally occurring antigens, portions of naturally occurring antigens, or other variants thereof.

Polynucleotides of the present invention may be isolated by screening a *M. vaccae* genomic DNA library as described below in Example 1. Alternatively, polynucleotides encoding *M. vaccae* epitopes may be obtained by screening an appropriate *M. vaccae* cDNA or genomic DNA library for DNA sequences that hybridize to degenerate oligonucleotides derived from amino acid sequences of isolated epitopes. Suitable degenerate oligonucleotides may be designed and synthesized, and the screen may be performed as described, for example in Sambrook *et al. Molecular cloning: a laboratory manual.* CSHL Press: Cold Spring Harbor, NY, 1989. Polymerase chain reaction (PCR) may be employed to isolate a nucleic acid probe from genomic DNA, or a cDNA or genomic DNA library, using techniques well known in the art. The library screen may then be performed using the isolated probe.

Regardless of the method of preparation, the epitopes described herein have the ability to induce an immunogenic response. More specifically, as discussed above, the epitopes have the ability to induce cell proliferation and/or cytokine production (for example, interferon-γ and/or interleukin-12 production) in T cells, NK cells, B cells or macrophages derived from a mycobacteria-immune individual.

The selection of cell type for use in evaluating an immunogenic response to an epitope will depend on the desired response. For example, interleukin-12 production is most readily evaluated using preparations containing T cells, NK cells, B cells and/or macrophages derived from mycobacteria-immune individuals which may be prepared using methods well known in the art. For example, a preparation of peripheral blood mononuclear cells (PBMCs) may be employed without further separation of component cells. PBMCs may be prepared, for example, using density centrifugation through Ficoll™ (Winthrop Laboratories, NY). T cells for use in the assays described herein may be purified directly from PBMCs. Alternatively, an enriched T cell line reactive against mycobacterial proteins, or T cell clones reactive to individual mycobacterial proteins, may be employed. Such T cell clones may be generated by, for example, culturing PBMCs from mycobacteria-immune individuals with mycobacterial proteins for a period of 2-4 weeks. This allows expansion of only the mycobacterial protein-specific T cells, resulting in a line composed solely of such cells. These cells may then be cloned and tested with individual proteins, using methods well known in the art, to more accurately define individual T cell specificity. Assays for cell proliferation or cytokine production in T cells, NK cells, B cells or macrophages may be performed, for example, using the procedures described below.

Among the immunogenic epitopes, polypeptides and/or polynucleotides of the present invention, those having superior therapeutic properties may be distinguished based on the magnitude of the responses in the above assays and based on the percentage of individuals for which a response is observed. In addition, epitopes having superior therapeutic properties will not stimulate cell proliferation or cytokine production *in vitro* in cells derived from more than about 25% of individuals that are not mycobacteria-immune, thereby eliminating responses that are not specifically due to mycobacteria-responsive cells. Thus, those antigens that induce a response in a high percentage of T cell, NK cell, B cell or macrophage preparations from mycobacteria-immune individuals (with a low incidence of responses in cell preparations from other individuals) have superior therapeutic properties.

Epitopes with superior therapeutic properties may also be identified based on their ability to diminish the severity of *M. tuberculosis* infection, or other mycobacterial infection, in experimental animals, when administered as a vaccine. Suitable vaccine preparations for use in experimental animals are described in detail below.

Portions and other variants of the inventive polypeptides may be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. *See* Merrifield, *J. Am. Chem. Soc.* 85:2149-2154, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems, Inc. (Foster City, CA), and may be operated according to the manufacturer's instructions. Variants of a native epitope may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis. Sections of the DNA sequence may also be removed using standard techniques to permit preparation of truncated polypeptides.

The present invention also provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known antigen, such as the *M. tuberculosis* 38 kDa antigen described in Andersen and Hansen, *Infect. Immun.* 57:2481-2488, 1989, together with variants of such fusion proteins. In a related aspect, genetic constructs comprising a first and a second inventive polynucleotide, or an inventive polynucleotide and a known polynucleotide, are also provided. Preparation of genetic constructs comprising multiple epitopes of the present invention and expression of the corresponding recombinant proteins is detailed below in Example 4.

In general, a polynucleotide encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide fold into its secondary and

tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea *et al.*, *Gene* 40:39-46, 1985; Murphy *et al.*, *Proc. Natl. Acad. Sci. USA 83*:8258-8262, 1986; and U.S. Patent Nos. 4,935,233 and 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference. The ligated DNA sequences encoding the fusion proteins are cloned into suitable expression systems using techniques known to those of ordinary skill in the art.

In another aspect, the present invention provides methods for using one or more of the inventive polypeptides or fusion proteins (or polynucleotides encoding such polypeptides or fusion proteins) to induce protective immunity against disorders, such as tuberculosis, in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease or infection. In other words, protective immunity may be induced to prevent or treat disorders.

In related aspects, the *M. vaccae* polynucleotides and polypeptides of the present invention may be employed to activate T cells and NK cells; to stimulate the production of cytokines (in particular Th1 class of cytokines) in human PBMC; to produce anti-epitope antibodies; to induce long-term memory cells and/or to enhance an immune response against an antigen.

For use in such methods, the polypeptide, fusion protein or polynucleotide is generally present within a composition, such as a pharmaceutical composition or an immunogenic composition. Compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable

carrier. Immunogenic compositions may comprise one or more of the above polypeptides or fusion proteins and an immunostimulant, such as an adjuvant or a liposome, into which the polypeptide or fusion protein is incorporated. Such compositions may also contain other antigens and/or polypeptides, either incorporated into a fusion protein or present as a separate polypeptide. Examples of polypeptides which may be usefully employed in combination with the polypeptides of the present invention include other mycobacterial antigens and flt3 ligands, as disclosed in US Patent 5,554,512, the disclosure of which is hereby incorporated in its entirety.

Alternatively, a composition of the present invention may contain a polynucleotide encoding one or more polypeptides as described above, such that the polypeptide is generated *in situ*. In such compositions, the polynucleotide may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacterial and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA/RNA sequences for expression in the patient (such as a suitable promoter and terminator signal). Bacterial delivery systems involve the administration of a bacterium (such as Bacillus Calmette-Guerin) that expresses an immunogenic epitope of the polypeptide on its cell surface. In a preferred embodiment, the DNA and/or RNA may be introduced using a viral expression system (*e.g.*, vaccinia or other poxvirus, retrovirus, or adenovirus), that may involve the use of a non-pathogenic, or defective, replication competent virus. Techniques for incorporating DNA and/or RNA into such expression systems are well known in the art. The DNA may also be "naked," as described, for example, in Ulmer *et al.*, *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells. Methods for the administration of polynucleotide sequences comprising DNA and/or RNA include those disclosed in US Patent Nos. 5,580,859 and 5,589,466.

A polynucleotide composition as described above may be administered simultaneously with or sequentially to either a polypeptide of the present invention or a known antigen, for example a mycobacterial antigen, such as the 38 kDa antigen from *M. tuberculosis*. For example, administration of DNA encoding a polypeptide of the present invention, may be

followed by administration of an antigen in order to enhance the protective immune effect of the composition.

Routes and frequency of administration of the inventive compositions, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunization using *M. bovis* BCG. In general, the compositions may be administered by injection (*e.g.*, intradermal, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Between 1 and 3 doses may be administered for a 1-36 week period. Preferably, 3 doses are administered, at intervals of 3-4 months, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or polynucleotide that, when administered as described above, is capable of raising an immune response in a patient sufficient to protect the patient from mycobacterial infection for at least 1-2 years. In general, the amount of polypeptide present in a dose (or produced *in situ* by the polynucleotide in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 ml to about 5 ml.

While any suitable carrier known to those of ordinary skill in the art may be employed in the compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic galactide) may also be employed as carriers for the compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of immunostimulants, such as an adjuvant, may be employed in the compositions of this invention to non-specifically enhance the immune response. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a non-specific stimulator of immune responses, such as lipid A, *Bordetella pertussis*, *M. tuberculosis*, or, as discussed below, *M. vaccae*. Suitable

adjuvants are commercially available as, for example, Incomplete Freund's Adjuvant (IFA) and Complete Freund's Adjuvant (Difco Laboratories, Detroit, MI), and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ). Other suitable adjuvants include alum, biodegradable microspheres, monophosphoryl lipid A and Quil A.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

CLONING AND SELECTION OF IMMUNOGENIC *M. VACCAE* EPITOPES

M. vaccae (ATCC Number 15483, Manassas, VA) was cultured in medium 90 (yeast extract, 2.5 g/l; tryptone, 5 g/l; glucose, 1 g/l) at 37 °C for four days. Genomic DNA was isolated from these cells following standard protocols and then digested with restriction endonuclease *Sau*3A under conditions that produced DNA fragments of approximately 0.25 kb. The fragments were purified using the QIAquick PCR clean-up system (Qiagen, Venlo, The Netherlands).

To express the cloned *M. vaccae* DNA in three different reading frames, the pcDNA3 expression vector (Invitrogen, Carlsbad, CA) was modified by insertion of a human growth hormone signal peptide (to facilitate recombinant protein secretion) amplified with three different 3' primers. These primers allowed the insertion of one or two extra base pairs into the PCR product to shift the reading frame of the expressed polypeptide. The primers were AD105 (human growth hormone 5' primer; SEQ ID NO: 1) and the three human growth hormone (hGH) 3' primers AD106, AD107 and AD108 (SEQ ID NO: 2-4, respectively). From these PCR fragments, most of the hGH sequence downstream of the leader sequence cleavage site was removed by digestion with the restriction endonuclease *Bsg*II. The hGH PCR fragments were then cloned into the pcDNA3 expression vector following digestion with the restriction endonucleases *Hind*III and *Bam*HI. The nucleotide sequences of the inserted fragments are given in SEQ ID NO: 5-7, with the corresponding amino acid sequences being provided in SEQ ID NO: 61-63, respectively. Three expression libraries (one for each of the three reading frames) were constructed by cloning the 0.25 kb *M. vaccae* PCR fragments, prepared as described above, into the *Bam*HI cloning site of the chimeric pcDNA3/human growth hormone vectors (pcDNA3-

hGH1', pcDNA3-hGH2' and pcDNA3-hGH3'). Replica lift master plates were made of bacterial colonies transformed with the library constructs and stored. Plasmid DNA, prepared from these colonies, was divided into 500 pools, each containing DNA from 40 to 50 plasmids. The DNA was transfected into COS7 cells using lipofectamine (BRL Life Technologies, Gaithersburg MD) and the immunogenic properties of the products of each group were determined by a spleen cell assay, wherein the production of IFN-γ in cultures of spleen cells obtained from mice primed with heat-killed *M. vaccae* was determined by ELISA as described below.

Plasmid pools that encoded recombinant polypeptides eliciting an immune response (as determined by the ability to increase IFN-γ production in the spleen cell assay), were subdivided into smaller pools containing 10 plasmids each and these pools were again transfected into COS7 cells. The culture supernatants of these cells were subjected to the spleen cell assay as described above.

After three rounds of screening, 120 plasmids were identified that encoded recombinant polypeptides stimulating spleen cells of heat-killed *M. vaccae*-immunized mice to produce IFN-γ. The 120 supernatants of COS7 cells transfected with these plasmids were screened in two additional assays, namely the mouse memory assay and the human peripheral blood mononuclear cell (PBMC) assay. In the mouse long-term memory assay, mice were injected with a sub-lethal dose of 10^4 colony forming units (CFU) of *M. tuberculosis*. After 4 weeks, the mice were treated with antibiotics for a further 4 weeks to cure them of *M. tuberculosis* infection, followed by a resting period of 4 weeks. A second injection of live *M. tuberculosis* (5×10^5 CFU) was given before the immunogenicity of the plasmid products was measured four days later using the spleen cell assay described above.

In the PBMC assay, the 120 supernatants of COS7 cells transfected with the plasmids were screened for the ability to induce T-cell proliferation and IFN-γ production in peripheral blood cells from mycobacteria-immune human donors. These donors were known to be PPD (purified protein derivative from *M. tuberculosis*) positive and their T cells were shown to proliferate and produce IFN-γ in response to PPD. Donor PBMCs and COS7 supernatants were cultured in medium comprising RPMI 1640 supplemented with 10% (v/v) autologous serum,

penicillin (60 μg/ml), streptomycin (100 μg/ml), and glutamine (2 mM). After 3 days, 50 μl of medium was removed from each well for the determination of IFN-γ levels, as described below. The plates were cultured for a further 4 days and then pulsed with 1 μCi/well of tritiated thymidine for 18 hours, harvested and tritium uptake determined using a scintillation counter. Supernatants that stimulated proliferation in two replicates at levels two-fold greater than the proliferation observed in cells cultured in medium alone were considered positive.

IFN-γ was measured using an enzyme-linked immunosorbent assay (ELISA) as follows. ELISA plates were coated with a mouse monoclonal antibody directed to human IFN-γ (Endogen, Wobural, MA) by incubating the wells with 1 μg/ml antibody in phosphate-buffered saline (PBS) for 4 hours at 4°C. Wells were blocked with PBS containing 0.2% Tween 20 for 1 hour at room temperature. The plates were then washed four times in PBS/0.2% Tween 20, and samples diluted 1:2 in culture medium in the ELISA plates were incubated overnight at room temperature. The plates were again washed, and a biotinylated polyclonal rabbit anti-human IFN-γ serum (Endogen), diluted to 1 μg/ml in PBS, was added to each well. The plates were then incubated for 1 hour at room temperature, washed, and horseradish peroxidase-coupled avidin A (Vector Laboratories, Burlingame, CA) was added at a 1:4,000 dilution in PBS. After a further 1 hour incubation at room temperature, the plates were washed and orthophenylenediamine (OPD) substrate added. The reaction was stopped after 10 minutes with 10% (v/v) HCl. The optical density (OD) was determined at 490 nm. Supernatants that resulted in both replicates giving an OD two-fold greater than the mean OD from cells cultured in medium alone were considered positive.

From the results of these two assays, 59 plasmids were identified that encoded recombinant polypeptides containing immunogenic determinants, or epitopes. These epitopes were found to elicit an immune response in mice and humans, and are cross-reactive with *M. tuberculosis* immunogenic determinants inducing long term responses. These plasmids were tested for their ability to induce protective immunity in the mouse model of tuberculosis as follows. Each plasmid (100 μg of DNA) was injected IM in the tibialis anterior of anaesthetized mice, three times every three weeks. After nine weeks, the mice were challenged with *M. tuberculosis* (5 X 10^5 CFU). Organ homogenates from lungs and spleens were prepared in

week 12 and plated out on 7H9 medium supplemented with oleic acid-albumin-dextrose-catalase (OADC) to determine the number of CFU present in each homogenate. Results were recorded after a two-week incubation period.

Using the protocols described above, eight plasmids containing immunogenic epitopes were selected. After identification of the putative open reading frames (ORFs) in these constructs, the *M. vaccae* fragments comprising only the ORF-portion were sub-cloned into pcDNA3-hGH' as described above. These plasmids were called DNA5, DNA9, DNA26, DNA27, DNA29, DNA37, DNA44 and DNA45. Three ORFs, referred to as A, B and C, were identified in DNA9. Open reading frames B and C were in the reverse orientation and were discarded. ORF A was cloned separately and the resulting plasmid was called DNA9A. The determined genomic DNA sequences of the inserts of DNA5, DNA9A, DNA26, DNA27, DNA29, DNA37, DNA42, DNA44 and DNA45 are given in SEQ ID NO: 13-21, respectively, with the amino acid sequences of the corresponding ORFs being provided in SEQ ID NO: 69-77, respectively. More than one epitope was identified in the inserts of the plasmids DNA5 and DNA27. These epitopes were not separated by cloning and were tested as multiple epitopes in all the assays. The determined genomic DNA sequences of epitope 1, epitope 2 and epitope 3 of DNA5, and of epitope 1 and epitope 2 of DNA27 are given in SEQ ID NO: 8-12, respectively, with the corresponding amino acid sequences being provided in SEQ ID NO: 64-68, respectively. The determined epitope DNA sequences were compared to sequences in the EMBL DNA database using the FASTA computer algorithm. The corresponding protein sequences (DNA translated to protein in each of 6 reading frames) were compared to sequences in the SwissProt database using the computer algorithm FASTX. Comparisons of DNA sequences provided in SEQ ID NO: 8-21 to sequences in the EMBL DNA database (using FASTA) and amino acid sequences provided in SEQ ID NO: 64-77 to sequences in the SwissProt database (using FASTX) were made as of March 21, 1999.

The amino acid sequences of DNA5 epitope 2, DNA27 epitope 1, DNA9A, DNA29, DNA37, DNA44 and DNA45 (provided in SEQ ID NO: 65, 67, 70, 73, 74, 76 and 77, respectively) were found to have less than 50% identity, determined as described above, to sequences in the SwissProt database using FASTX. The amino acid sequences of DNA5 epitopes 1 and 3 (provided in SEQ ID NO: 64 and 66, respectively) were found to have less than

75% identity, determined as described above, to sequences in the SwissProt database using FASTX. No matches were found to the amino acid sequence of DNA27 epitope 2 and DNA26 (provided in SEQ ID NO: 68 and 71, respectively). Table 1, below, shows the results of the comparison of the inventive amino acid sequences with those in the SwissProt database using FASTX as described above, wherein "No. of identical residues" represents the number of identical residues within the aligned portion.

TABLE 1

	SEQ ID NO:	Length (residues)	Length of alignment (residues)	No. of identical residues	% identity
DNA5, epitope 1	64	13	11	8	61
DNA5, epitope 2	65	32	31	10	32
DNA5, epitope 3	66	26	25	14	53
DNA9A	70	75	68	24	32
DNA26	71	97	No Hits		
DNA27, epitope 1	67	38	30	16	42
DNA27, epitope 2	68	11	No Hits		
DNA29	73	46	40	17	37
DNA37	74	87	80	26	32
DNA44	76	44	35	17	38
DNA45	77	59	52	21	35

EXAMPLE 2

EXPRESSION OF RECOMBINANT EPITOPES IN PROKARYOTIC AND EUKARYOTIC CELLS

Epitope DNA was subcloned into vectors for expression of polypeptides in bacterial and eukaryotic cells. The bacterial expression vector was a modified pET16 vector (Novagen, Madison, WI). Inserts from all the plasmids except for DNA9, were amplified with primers AD136 and AD133 (SEQ ID NO: 22 and 23, respectively) and cloned by blunt-end ligation into the pET16 vector that was *Eco*RI-digested and end-filled with DNA polymerase *Pfu*I (Stratagene, La Jolla CA). The insert of DNA9A was amplified with primers AD250 and

AD251 (SEQ ID NO: 24 and 25, respectively) and cloned into the pET16 vector as described above.

To express the polypeptides in eukaryotic cells, the pcDNA3 vector (Invitrogen) was modified to include a histidine tag at the 3' end of the cloning site. This was done by cloning the double-stranded oligonucleotide AD180/AD181 into pcDNA3 digested with *Bam*HI and *Eco*RI. The sequences of oligonucleotides AD180 and AD181 are given in SEQ ID NO: 26 and 27, respectively. Plasmid inserts were amplified with the hGH-specific N-terminus 5' primer AD134 (SEQ ID NO: 28) and an epitope-specific 3' end primer, using the pcDNA3-hGH' constructs as DNA template. The sequences of the epitope-specific 3' primers AD151 (DNA5), AD153 (DNA26), AD154 (DNA27), AD155 (DNA29), AD158 (DNA42), AD159 (DNA44), AD160 (DNA45), AD167 (DNA37) and AD182 (DNA9) are listed in SEQ ID NO: 29-37, respectively.

This vector was again modified to remove excess sequence (42 nucleotides) between the hGH leader sequence and the expressed sequence, so that the hGH' sequence in this construct was reduced to the leader sequence and the first 5 N-terminal amino acids of the hGH sequence only. Using the pcDNA3-hGH3' construct as DNA template, the shortened fusion partner was amplified by PCR using primers AD105 (SEQ ID NO: 1) and AD222 (SEQ ID NO: 38). Cloning into pcDNA3-His was done at the *Hind*III and *Bam*HI sites and the resulting construct was called pcDNA3-hGHls/His. The determined DNA sequence of the hGH-fusion partner cloned into pcDNA3-hGH-ls is given in SEQ ID NO: 39 and the corresponding amino acid sequence in SEQ ID NO: 78. The construct consisting of the insert from DNA9A was prepared by PCR amplification using primers AD223 and AD226 (SEQ ID NO: 40 and 41, respectively).

EXAMPLE 3

IMMUNOGENICITY OF RECOMBINANT EPITOPE CONSTRUCTS

This example describes the results of immunogenicity studies performed with eight selected recombinant epitopes in either DNA or recombinant polypeptide form.

A. Stimulation of Human Peripheral Blood Mononuclear Cells (PBMC) to proliferate and secrete Interferon gamma (IFN-γ) *in vitro*

The recombinant epitopes (1 and 10 μg) expressed by the pET16 bacterial expression system were cultured with human PBMC at 37 °C. After 48 hours, IFN-γ secretion was measured by enzyme-linked immunoassay (ELISA) following standard procedures. Parallel cultures were pulsed with tritiated thymidine and DNA synthesis was used to assess PBMC proliferation. For comparison, cells were also cultured with Purified Protein Derivative (PPD) from *M. tuberculosis* and with PBS as a negative control.

As shown in Table 2, all recombinant epitopes have the ability to stimulate IFN-γ production in at least some PBMC samples. Of the 12 PBMC samples tested, 10 were PPD positive, *i.e.*, the PBMCs from these samples produced IFN-γ when cultured with PPD, and 2 were PPD-negative. PBMC responses were considered positive when the amount of IFN-γ produced was at least 3-fold higher than the IFN-γ produced by the PBS control samples. Recombinant epitopes 5 (corresponding to DNA5) and 44 (corresponding to DNA44) stimulated IFN-γ production in 100% of the PPD^+ samples. Recombinant epitope 27 (corresponding to DNA27) stimulated IFN-γ production in 80% of the PPD^+ samples. Recombinant epitopes 26 and 37 (corresponding to DNA26 and DNA37, respectively) stimulated IFN-γ production in 70% of the PPD^+ samples, whereas epitope 45 (corresponding to DNA45) stimulated 20% PPD^+ of the PBMC samples. PBMCs from PPD^- samples did not respond significantly to any of the recombinant epitopes. This demonstrates that the epitopes are immunogenic in humans and trigger a recall response in samples from donors that were previously exposed to mycobacteria.

TABLE 2

Stimulation of IFN-γ production in human PBMC by recombinant epitopes

Human PBMC	PBS control	PPD control	Recombinant Epitopes					
			26	37	44	45	5	27
G97022	<0.1	0.16	0.3	0.3	0.4	<0.1	0.5	0.1
G97037	<0.1	0.3	0.3	0.3	0.8	0.2	0.3	0.3
G97001	<0.1	4.5	0.6	1	3.5	0.2	1.8	1.7
G97008	<0.1	4.4	0.16	0.5	4	<0.1	0.73	0.9
G97011	0.25	4.9	0.9	0.5	1.2	0.25	2.8	1.2
G97030	<0.1	1.8	0.5	0.2	3.5	0.1	1.8	3
G97033	0.12	4.5	0.5	0.25	3.4	0.2	1.7	1
G97010	<0.1	>4	>4	>4	>4	1	>4	>4
G97028	<0.1	>4	>4	>4	>4	1.2	>4	>4
G97020	<0.1	1	0.3	0.25	>4	<0.1	1.5	0.5
G97032	<0.1	>4	0.5	1.2	>4	<0.1	1.4	0.5
G97035	<0.1	3.5	0.4	3.5	>4	<0.1	1	1

* Results are expressed as IFN-γ in ng/ml

Immunogenicity of the epitopes in humans was further demonstrated by the proliferative response of the human PBMC samples to both PPD and recombinant epitopes. The ability of the recombinant epitopes to stimulate PBMC proliferation was expressed as a stimulation index. A proliferation stimulus is considered positive when it is 5 times greater than the mean background proliferation produced by the medium-only control. As shown in Table 3, all recombinant epitopes were found to have the ability to stimulate PBMC proliferation in at least some of the human PBMC samples. Recombinant epitopes 26 and 27 stimulated PBMC proliferation in 92% of the samples, while recombinant epitopes 5, 37 and 44 stimulated proliferation in 83% of the

samples. Epitope 45 stimulated PBMC proliferation in 17% of the samples. Stimulation of PBMC by PPD was 83%.

TABLE 3

Stimulation of PMBC proliferation

Human PBMC	Recombinant epitopes						
	PPD	5	26	27	37	44	45
G97022	5*	12	14	3	20	20	1
G97037	35	12	25	20	15	30	1
G97001	5	6	6	5	8	7	1
G97008	60	20	30	15	40	60	2
G97011	40	33	30	27	30	30	3
G97030	100	140	120	140	120	140	30
G97033	20	12	12	11	10	15	1
G97010	2	4	2	6	2	4	2
G97028	60	48	60	40	55	52	12
G97020	10	10	10	8	10	10	1
G97032	45	30	35	33	38	42	2
G97035	3	4	5	6	3	4	2

* Results of human PBMC proliferation are expressed as Stimulation Index.

B. Immunization of mice with DNA epitopes

Protective immunity against subsequent infection with *M. tuberculosis* was induced in BALB/cByJ mice after injection of DNA encoding eight of the recombinant epitopes in pcDNA-hGH'/His or pcDNA3-hGHls/His constructs.

Induction of protective immunity was considered positive when a mean 0.5 log reduction in CFU in lung homogenates, compared to the mean CFUs from non-immunized control mice,

was observed following subsequent infection with *M. tuberculosis*. A plasmid without an insert was used as control. The reduction in CFUs after epitope DNA immunization was also compared with the known immunogenicity of *M. bovis* BCG. The results clearly show a reduction in CFUs in all the mice tested, suggesting the induction of protective immunity by the recombinant epitope DNA. In six of the groups, the reduction in CFUs was greater than 50% and in three of the groups the reduction was comparable to that induced by injection with *M. bovis* BCG.

TABLE 4

Protective immunity in mice induced by genetic immunization with eight pcDNA-hGH'/His and pcDNA3-hGHls/His constructs

Epitope construct	SEQ ID NO:	Number of Mice	Number of mice with reduced CFUs	% Mice with Reduced CFUs
Control plasmid		14	2	14
DNA5	13	11	4	36
DNA9	14	13	7	55
DNA26	15	10	7	70
DNA27	16	13	7	55
DNA29	17	13	7	55
DNA37	18	13	8	62
DNA44	20	13	6	46
DNA45	21	13	8	62
M. bovis BCG		23	17	74

The induction of cytotoxic T lymphocytes (CTL), cytokines (IFN-γ, IL-4, IL-6 and IL-10), and proliferative and antibody responses upon genetic immunization with eight pcDNA-hGH'/His or pcDNA3-hGHls/His constructs were assessed as follows.

CTL assay:

Cytolytic (CTL) activity in spleen cells of DNA-immunized BALB/cByJ mice was measured following a standard two-step procedure using the MHC haplotype matching target cells, BALB-3T3 (ATCC No. CRL-163, American Type Culture Collection, Manassas, VA). Target cells were prepared by transfecting BALB/3T3 cells with eight pcDNA-hGH'/His or pcDNA3-hGHls/His epitope DNA constructs. Stably transfected cell lines were produced by geneticin selection (G418; Gibco BRL Life Technologies) and single cells were isolated by limiting dilution. Clones expressing epitopes were selected by RT-PCR using primers AD105 and AD181 (SEQ ID NO: 1 and 27, respectively). Spleen cells of DNA-immunized mice were cultured in cDMEM enriched with 10% FCS in the presence of mytomycin-treated BALB-3T3 cells transfected with matching epitope DNA to re-stimulate cytotoxic T cells *in vitro*. Cultures were incubated at 37 °C under 10% CO_2 for 6 days. Cytolytic activities were monitored by incubating a fraction of each stimulated cell culture with DNA-matched target cells that were pulsed with ^{51}chromium, and measuring ^{51}chromium release in the supernatant of cell cultures. As shown in Table 5, specific CTL activity was detected in the spleens of mice immunized with four of the DNA constructs tested.

Cytokine and proliferative responses:

Cytokine production and proliferative responses of spleen cells from DNA-immunized BALB/cByJ mice were assessed following *in vitro* re-stimulation with recombinant epitopes. Cytokine and proliferative responses were measured by ELISA and 3H-thymidine pulse, respectively, as described above. As shown in Table 5, spleen cells from the six groups tested produced the Th1 cytokine IFN-γ. No Th2 cytokines (e.g. IL-4, IL-6 and IL-10) were detected in supernatants of stimulated cells. Proliferative responses were low and detected in spleen cells from two immunized groups only.

Antibody responses

Blood samples from three DNA-immunized BALB/cByJ mice were collected two weeks after the last DNA injection and sera were prepared according to standard procedures. The presence of anti-epitope antibodies was determined by ELISA. The wells of a microtitre plate

were coated with 500 ng of recombinant epitope. Antibody titers were measured by adding serial dilutions of serum into the wells. Bound antibodies were detected according to ELISA procedures as described above. As shown in Table 5, anti-epitope antibodies were detected in two blood samples tested. ELISA assays were also performed to determine whether the antibodies belonged to the IgG1 or IgG2a subclasses, using standard protocols. The results showed that the antibodies belonged to the IgG2a subclass, which is characteristic of a Th1 antibody response.

The data summarized in Table 5 indicate that immunization with epitope DNA induced an immune response in mice. Furthermore, the cellular and humoral responses detected in the DNA-immunized mice demonstrated that a Th1 response was generated.

TABLE 5

Cytotoxic lymphocyte induction, cytokine responses, proliferation and antibody production induced in mice by genetic immunization with eight pcDNA-hGH'/His or pcDNA3-hGHls/His constructs.

Epitope constructs	**SEQ ID NO:**	**CTL induction** (% Specific lysis)*	**Cytokine responses** (IFN-γ in ng/ml)**	**Proliferation** (Stimulation Index)	**Antibodies** (titer)
DNA5	13	30	15	not detected	not detected
DNA9A	14	10	NT***	NT	NT
DNA26	15	not detected	30	7	not detected
DNA27	16	not detected	33	3	1/100
DNA29	17	not detected	NT	NT	NT
DNA37	18	not detected	18	not detected	not detected
DNA44	20	25	23	not detected	1/100
DNA45	21	20	12	not detected	not detected

* Data shown is the mean % lysis from spleen cells of three mice. Non-specific lysis of control cells was deducted.

** Data shown is the mean IFN-γ in ng/ml obtained from triplicates of spleen cell cultures from three mice. Background IFN-γ produced by control cells was 5-7 ng/ml.

*** NT=Not Tested

EXAMPLE 4

CLONING STRATEGY FOR *M. VACCAE* MULTI-EPITOPE CONSTRUCTS

The eight epitopes assayed in Example 4 were assembled to form multi-epitope constructs, of fusion proteins. Specifically, the DNA was amplified with primers containing a *BglII* 5'-extension and *Bam*HI 3'-extension and was sequentially cloned into the *Bam*HI site of pcDNA3/hGHls/His. The primers were AD223, AD226, AD229, AD230, AD231, AD232, AD233, AD234, AD235, AD236, AD256, AD258, AD259, AD260, AD261 and AD262 (SEQ ID NO: 40-55, respectively).

The insert of plasmid DNA9A was cloned first into the *Bam*HI site of pcDNA3-hGHls/His. The *Bam*HI site of the vector was reconstituted at the 3' end of the cloning junction only and all other inserts except DNA5 were sequentially cloned into the same site. The insert of plasmid DNA5 was cloned last by blunt ligation into the end-filled *Bam*HI site of pcDNA3-hGHls/His. Following this protocol, various combinations of epitopes were cloned into the pcDNA3-hGHls/His vector. The determined DNA sequences of three multi-epitope constructs consisting of 8-mer multi-epitopes (called ME/A, ME/B and ME/D) are shown in SEQ ID NO: 56-58, respectively, and the corresponding amino acid sequences in SEQ ID NO: 79-81, respectively. Each one of these multi-epitope constructs includes each one of the 8 epitopes, but in a different order. The amino acid sequence for ME/D provided in SEQ ID NO: 81 includes the human growth hormone signal peptide added to enable expression of soluble secreted recombinant protein from eukaryotic cells as described above in Example 1 (amino acids 1-31 of SEQ ID NO: 81). Amino acids 32 and 33 of SEQ ID NO: 81 are a concatenating linker used to connect the signal peptide to the epitope 9A sequence. The amino acid sequence of the ME/D fusion polypeptide minus the signal peptide and this linker is provided in SEQ ID NO: 116, with the corresponding DNA sequence being provided in SEQ ID NO: 115.

For expression of multi-epitope recombinant proteins in bacteria, the inserts of plasmids ME/A, ME/B and ME/D were subcloned into the modified expression vector pET16. All 8-mer epitope DNA combinations had DNA9A and DNA5 at the 5' and 3' end, respectively. The plasmid inserts were amplified using primers AD272 and AD273 (SEQ ID NO: 59 and 60,

respectively) and the purified amplified fragments cloned by blunt-end ligation into the pET16 vector that was *Eco*RI-digested and end-filled with DNA polymerase *Pfu*I (Stratagene). Recombinant protein was expressed using *E. coli* host cells according to the manufacturer's protocol and purified using standard protocols.

EXAMPLE 5

IMMUNIZATION OF MICE WITH *M. VACCAE* MULTI-EPITOPE CONSTRUCTS

This example illustrates the protective immunity against subsequent infection with *M. tuberculosis* in BALB/cByJ mice after injection of multi-epitope constructs in either DNA or recombinant polypeptide form.

BALB/cByJ mice were divided into three groups of six mice that received different treatments. Mice in Group 1 were immunized intraperitoneally with one dose of 500 µg *M. bovis* BCG or PBS. Group 2 mice were immunized three times intramuscularly in the *tibialis anterior* with 100 µg ME/D DNA or empty vector DNA at three week intervals. Mice in Group 3 were immunized intraperitoneally at three week intervals with either 1 or 2 doses of 50 µg recombinant ME/D in IFA, or 50 µg control protein in IFA. The control protein GV14B consisted of a non-naturally occurring protein derived from DNA encoding the *M. vaccae*-homologue of mycobacterial Elongation factor G and cloned into pET16g3 in reverse orientation.

Three weeks after the last immunization, the mice were challenged with live *M. tuberculosis* (5×10^5 CFU). Organ homogenates from lungs and spleens were prepared after a further three weeks and plated out on 7H9 medium supplemented with oleic acid-albumin-dextrose-catalase (OADC) to determine the number of CFU present in each homogenate. Results were recorded after a two-week incubation period.

Induction of protective immunity was considered positive when a mean 0.5 log reduction in CFU in lung and spleen homogenates, compared to the mean CFUs from non-immunized control mice, was observed following subsequent infection with *M. tuberculosis.* The reduction in CFUs after immunization with ME/D DNA or recombinant ME/D polypeptide was compared with the known immunogenicity of *M. bovis* BCG. The results (Fig. 1) show a reduction in

CFUs in the lungs and spleens from mice immunized with the ME/D DNA as well as the recombinant ME/D construct. The protective immunity of the ME/D DNA and the rME/D polypeptide demonstrated by the reduction in both lung and spleen CFUs was greater than the reduction in lung CFU after immunization with single epitope constructs (Table 4).

EXAMPLE 6

IMMUNOGENICITY OF *M. VACCAE* MULTI-EPITOPE CONSTRUCTS

This example describes the results of immunogenicity studies performed with three multi-epitope constructs in either DNA or recombinant polypeptide form.

A. Recombinant multi-epitope constructs ME/A, ME/B and ME/D stimulate mouse lymph node cells to proliferate and secrete IFN-γ *in vitro*

The recombinant multi-epitope constructs, or fusion proteins, rME/A, rME/B and rME/D were screened for their ability to induce T-cell proliferation and IFN-γ in murine lymph node cells. For this assay, BALB/cByJ mice were immunized subcutaneously in each footpad with 10 μg of the recombinant multi-epitope fusion proteins rME/A, rME/B or rME/C diluted in an equal volume of IFA. Mice from the control group received PBS in IFA. Mice were sacrificed after nine days and the lymph nodes removed. Lymph node cells were cultured in medium comprising DMEM supplemented with 10% (v/v) autologous serum, penicillin (60 μg/ml), streptomycin (100 μg/ml), and glutamine (2 mM) in the presence of 0, 0.125, 0.25 or 0.5 μM rME/A, rME/B or rME/D, as well as the control protein GV14B. After 3 days, 50 μl of medium was removed from each well for the determination of IFN-γ levels, as described above. The plates were cultured for a further 4 days and then pulsed with 1 μCi/well of tritiated thymidine for 18 hours. Cells were harvested and tritium uptake determined using a scintillation counter. Supernatants that stimulated proliferation in two replicates at levels two-fold greater than the proliferation observed in cells cultured in medium alone were considered positive.

Results from the murine proliferation experiments are shown in Figs. 2A-D. All three of the recombinant multi-epitope constructs, or fusion proteins, induced a proliferative response in lymph node cells from immunized mice. The levels of proliferation induced by the three

recombinant multi-epitope constructs rME/A, rME/B and rME/D (Fig. 2A, B and C, respectively) were similar, showing that the constructs were antigenically identical. No proliferation was obtained from control mice immunized with PBS (Fig. 2D).

The levels of IFN-γ secreted by stimulated lymph node cells from mice immunized with rME/A, rME/B or rME/D are shown in Fig. 3A-C, respectively. All three recombinant multi-epitope constructs stimulated IFN-γ secretion by lymph node cells, with the highest levels stimulated with rME/B (Fig. 3B). Cells from control mice stimulated with PBS secreted undetectable amounts of IFN-γ (Fig. 3D). These results indicate that immunization with the multi-epitope constructs induced a Th1 immune response in the mice.

B. Recombinant multi-epitope construct ME/D and ME/D DNA stimulate lymph node and spleen cells from mice immunized by different routes to proliferate and secrete IFN-γ *in vitro*

In these experiments, lymph node or spleen cells from mice immunized subcutaneously, intraperitoneally or intramuscularly with the recombinant multi-epitope construct rME/D or the DNA form of the multi-epitope construct ME/D were stimulated to induce T-cell proliferation and IFN-γ production. BALB/cByJ mice were immunized either subcutaneously in each footpad with one dose of 10 μg rME/D in IFA, intraperitoneally with one dose of 50μg rME/D in IFA, or intramuscularly with three doses at 3 week intervals with 100 μg ME/D DNA. Control mice were immunized with PBS by the three different immunization routes. After nine days, mice immunized by the subcutaneous and intraperitoneal routes were sacrificed and the lymph nodes (subcutaneous immunization) or spleen cells (intraperitoneal immunization) removed. Spleen cells from mice immunized by intramuscular injection were harvested 15 days after the last immunization. Proliferation and IFN-γ production by these cells were determined as described above.

Results from these experiments are presented in Fig. 4 and Fig. 5. In Fig. 4A, specific proliferative responses by lymph node and spleen cells from mice immunized with rME/D or ME/D DNA are shown. In comparison, Fig. 4B shows the low proliferation by cells from control mice. Similarly, lymph node and spleen cells from mice immunized with rME/D or

ME/D DNA were stimulated to secrete IFN-γ (Fig. 5A) while low levels of IFN-γ were secreted by lymph node and spleen cells from control mice immunized with PBS.

C. Single epitopes from multi-epitope constructs stimulate lymph node and spleen cells from mice immunized with recombinant multi-epitope construct rME/D or ME/D DNA by different routes to proliferate and secrete IFN-γ *in vitro*

In these experiments, lymph node and spleen cells from mice immunized with the recombinant multi-epitope construct rME/D or the DNA form of the multi-epitope construct, ME/D, by different immunization routes were re-stimulated with the recombinant form of the single epitopes DNA5, DNA9A, DNA26, DNA27, DNA29, DNA37, DNA44 and DNA45. The experimental procedure was the same as outlined above. Results from these experiments are shown in Fig. 6A-B and Fig. 7A-B. Specific proliferative responses and IFN-γ secretion were detected in cells re-stimulated with epitopes DNA5, DNA9A, DNA26, DNA37 and DNA44 (Fig. 6A and Fig. 7A). Proliferation and IFN-γ production by epitopes DNA27, DNA29 and DNA45 were seen in at least one immunization group. Low levels of proliferation and IFN-γ production were observed in cells from control mice immunized with PBS (Fig. 6B and Fig. 7B). The data indicates that the epitopes are all individually antigenic when presented to the immune system as part of a multi-component immunogen.

D. Cytokine production

The cytokine production by spleen cells from mice immunized with the DNA form of the multi-epitope construct ME/D and re-stimulated with rME/A or rME/D was determined as follows. BALB/cByJ mice were immunized intramuscularly with three doses at three week intervals of 100 μg ME/D DNA. Fifteen days after the last injection, mice were sacrificed and the spleen cells removed. The spleen cells were re-stimulated with rME/A, rME/D or the control protein GV14B and the supernatants screened for cytokine production following standard procedures. Cytokine production by the spleen cells is given in Table 6.

TABLE 6

Cytokines secreted by splenocytes from BALB/cByJ mice immunized with ME DNA

	IL-2*			IL-4*			IL-6*		
Plasmid	rME/A	rME/D	GV14B	rME/A	rME/D	GV14B	rME/A	rME/D	GV14B
ME/A	122	125	<50	42	56	39	147	196	<30
ME/B	267	200	<50	20	<10	<10	79	56	<30
ME/D	96	77	<50	13	<10	<10	131	98	<30
Control	<50	<50	<50	<10	<10	<10	<30	<30	<30

*Cytokine concentration measured in pg/ml, with a standard error of <10%

As shown in Table 6, IL-2 and IL-6 were secreted by spleen cells of mice stimulated with rME/A and rME/D. IL-2 is a cytokine secreted during a Th1-type immune response, providing further evidence that the multi-epitope constructs elicit a Th1-type immune response. The cytokine IL-6 plays an important role in the immunity of mice to tuberculosis (Ladel *et al.*, *Infect. Imm.* 65: 4843-4849, 1997). No secretion of IL-4, a Th2-type cytokine, was detected.

E. Antibody production

Blood samples from BALB/cByJ mice immunized with ME/D were collected two weeks after the last DNA injection and sera prepared according to standard procedures. The presence of anti-ME/D antibodies was determined by ELISA. As shown in Fig. 8B, high titers of IgG2a antibodies reacting with rME/A and rME/D were detected, but no IgG1 antibodies (Fig. 8A). The presence of IgG2a antibodies is characteristic of a Th1-type immune response.

F. Induction in mice of long-term memory responses by recombinant epitopes and recombinant multi-epitope construct rME/D.

The induction of long-term memory responses in mice infected with *M. tuberculosis* and immunized with either recombinant single epitopes rDNA5, rDNA9A, rDNA26, rDNA27, rDNA37, rDNA44 or rDNA45, or recombinant multi-epitope construct ME/D was determined as follows. In the mouse long-term memory assay, BALB/cByJ mice were injected with a sub-lethal dose of 10^4 colony forming units (CFU) of *M. tuberculosis*. After 4 weeks, the mice were

treated with antibiotics for a further 4 weeks to cure them of *M. tuberculosis* infection, followed by a resting period of 8 weeks. A second injection of live *M. tuberculosis* (5 X 10^5 CFU) was given before the immunogenicity of the recombinant constructs was measured three days later using the spleen cell assay described above. Spleen cells were stimulated with 2 μM of recombinant epitope or with 1, 0.33, 0.11, 0.03 or 0.01 μM rME/D. The levels of IFN-γ production determined in the spleen assay are shown in Figs. 9A-C. Spleen cells from control mice were stimulated with the unrelated protein GV14B (Fig. 9B). Other controls in this experiments included stimulation with medium only, 2 μg/ml ConA, 10 μg/ml PPD and 10 μg/ml *M. vaccae* (Fig. 9A). Recombinant ME/D stimulated memory T cells from mice infected with *M. tuberculosis* to produce large amounts of IFN-γ in a dose-dependent manner (Fig. 9B). The production of IFN-γ in this assay is indicative of the cross-reactivity of ME/D with *M. tuberculosis* antigens that induced long-term immune responses. Antigenic determinants cross-reacting with the *M. tuberculosis* antigens appears to be located on epitopes DNA5, DNA9A, DNA26, DNA27 and DNA44 (Fig. 9B).

EXAMPLE 7

<u>EFFECT OF STIMULATION OF HUMAN PERIPHERAL BLOOD MONONUCLEAR CELLS (PBMC) WITH RECOMBINANT SINGLE EPITOPES AND RECOMBINANT MULTI-EPITOPE CONSTRUCTS</u>

A. Stimulation of Human Peripheral Blood Mononuclear Cells (PBMC) to proliferate and secrete Interferon gamma (IFN-γ) *in vitro*

The recombinant epitopes and recombinant multi-epitope constructs expressed by the pET16 bacterial expression system were cultured with human PBMC at 37 °C. After 48 hours, IFN-γ secretion was measured by enzyme-linked immunoassay (ELISA) as described above. Parallel cultures were pulsed with tritiated thymidine and DNA synthesis was used to assess PBMC proliferation. Results of these experiments are shown in Figs. 10A-B and Figs. 11A-B. The recombinant multi-epitope constructs stimulated human PBMC to secrete IFN-γ and

proliferate (Figs. 10A and B, respectively). These responses were dose-dependent and of greater magnitude than the responses induced by the individual recombinant epitopes (Figs. 11A and B).

B. Stimulation of human PBMC by recombinant single epitopes and recombinant multi-epitope constructs rME/A and rME/D to secrete cytokines *in vitro*

Cytokine production of human PBMC were assessed following *in vitro* re-stimulation with recombinant single epitopes or recombinant rME/A or rME/D as follows. Cells were stimulated with 2 μM of the recombinant single epitopes rDNA5, rDNA9A, rDNA26, rDNA27, rDNA29, rDNA37, rDNA44 or rDNA45, or 0.5 μM rME/A or rME/D. Cells in the control groups were stimulated with 2 μM of the protein GV14B or 10 μg/ml PPD. Cytokine responses was measured by ELISA following standard procedures. As shown in Table 7, below, human PBMC stimulated with the recombinant single epitopes, or with rME/A or rME/D produced the Thl cytokines IFN-γ and TNF-α. These recombinant epitopes also induced secretion of IL-10. No IL-5, a Th2 cytokine, was detected in supernatants of stimulated cells. Low levels of cytokines were secreted in response to stimulation with the control antigen, and all cytokines tested were secreted by human PBMC after stimulation with PPD.

TABLE 7

Cytokines secreted by human PBMC after *in vitro* stimulation with recombinant single epitopes and rME

	Recombinant single epitopes								rME		Controls	
Cytokine	DNA 5	DNA 9A	DNA 26	DNA 27	DNA 29	DNA 37	DNA 44	DNA 45	rME/A	rME/D	GV14 B	PPD
IFN-γ	4.7	2.8	4.1	0.06	3.6	4.3	0.45	0.78.	4.4	3.2	<0.05	3.96
TNF-α	4.6	<0.05	1.2	0.1	3.5	2.3	0.5	<0.05	3.9	3.8	0.2	0.85
IL-10	0.75	<0.05	0.9	0.15	0.98	0.83	0.59	<0.05	1.17	1.12	0.07	0.34
IL-5	0.08	<0.05	<0.05	0.06	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05	0.06

EXAMPLE 8

STIMULATION OF LYMPHOCYTE PROLIFERATION IN CYNOMOLGUS MONKEYS AFTER IMMUNIZATION WITH RECOMBINANT rME/D.

Three groups each consisting of four cynomolgus monkeys were immunized to test the immunogenicity of the recombinant multi-epitope construct rME/D. Proliferation of lymphocytes was measured in a PBMC proliferation assay. The monkeys in Group I were immunized intradermally with PBS in incomplete Freund's adjuvant (IFA) in a total volume of 0.1 ml. Monkeys in Group II were immunized intradermally with 33 μg rME/D in IFA (total volume 0.1 ml) and monkeys in Group III were immunized intradermally with 10 μg rME/D in IFA (total volume 0.1 ml). Two immunizations were given, at week 0 and week 6. Blood samples were taken from each monkey 12 weeks after immunization.

Whole blood from each monkey was diluted 1:5 and stimulated with control medium (RPMI 1640 supplemented with 10% (v/v) autologous serum, penicillin (60 μg/ml), streptomycin (100 μg/ml), and glutamine (2 mM)) containing either the positive control phytohaemaglutinin (PHA, at 10 μg/ml), PPD (10 μg/ml), *M. vaccae* at 10 μg/ml, rME/D at 1 μg/ml or control recombinant protein GV-14B at 1 μg/ml in a total culture volume of 1 ml. The plates were cultured for 72 hours and then pulsed with 1 μCi/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a scintillation counter. Lymphocyte proliferation results are shown in Table 8.

TABLE 8

Lymphocyte proliferation in blood samples of cynomolgus monkeys stimulated with PHA, PPD, *M. vaccae*, rME/D or rGV-14B.

Group	**Monkey No.**	**PHA 10 μ/ml**	**PPD 10 μ/ml**	***M. vaccae* 10 μg/ml**	**rME/D 1 μg/ml**	**rGV-14B 1 μg/ml**
1	1	18*	1.3	0.73	1.36	0.77
	2	57	2.3	1.6	2.4	1.5
	3	32	1.6	1.5	1.6	1.0
	4	26	2.2	1.4	1.6	0.91

2	1	23	1.6	0.91	15	0.79
	2	70	2.1	2.0	20	2.2
	3	13	1.0	1.9	12	2.8
	4	40	3.1	2.5	25	3.3
3	1	35	1.2	1.9	18	2.4
	2	81	1.0	1.4	32	2.3
	3	29	1.4	2.2	15	1.3
	4	25	0.89	1.5	1.3	1.0

* Results of PBMC proliferation are expressed as Stimulation Index.

As shown in Table 8, the recombinant multi-epitope construct rME/D induced a proliferative response in PBMC cells from immunized monkeys in Groups II and III comparable to that of the positive control (PHA). No proliferation was recorded after stimulation with PPD, *M. vaccae* or rGV-14B.

EXAMPLE 9

CLONING OF ADDITIONAL *M. VACCAE* MULTI-EPITOPE CONSTRUCTS

Additional multi-epitope constructs were constructed by cloning the eight different epitopes assayed in Example 4. The epitopes were cloned into the vectors pcDNA3-hGHla/His and pET16 described in Example 1. The different epitopes were amplified using the primers listed in Table 9 and cloned into the vectors using *Bam*HI/*Xho*I restriction sites for the pcDNA3-hGHls/His constructs and *Eco*RI/*Xho*I restriction sites for the pET16 constructs.

The epitopes present in the different constructs are listed in Table 10, as well as the corresponding polynucleotide and polypeptide SEQ ID NOS: of each of the constructs. The epitopes cloned were DNA5 (SEQ ID NO: 13), DNA9A (SEQ ID NO: 14), DNA26 (SEQ ID NO: 15), DNA27 (SEQ ID NO: 16), DNA29 (SEQ ID NO: 17), DNA37 (SEQ ID NO: 18), DNA44 (SEQ ID NO: 20) and DNA45 (SEQ ID NO: 21).

TABLE 9

Primers used to amplify constructs MED1-MED8

Construct	SEQ ID NOS: of primer pair for modified pET16 vector		SEQ ID NOS: of primer pair for pcDNA3-hGHla/His vector	
	5' primer SEQ ID NO:	3'primer SEQ ID NO:	5' primer SEQ ID NO:	3' primer SEQ ID NO:
MED1	112	98	113	98
MED2	112	99	113	99
MED3	112	100	113	106
MED4	112	101	113	107
MED5	112	102	113	108
MED6	112	103	113	109
MED7	112	104	113	110
MED8	112	105	114	111

TABLE 10

Additional single and multi-epitope constructs

Polynucleotide SEQ ID NO:	Construct Name	Epitopes in Construct	Polypeptide SEQ ID NO:
82	MED1	DNA9A	90
83	MED2	DNA9A-DNA44	91
84	MED3	DNA9A-DNA44-DNA26	92
85	MED4	DNA9A-DNA44-DNA26-DNA45	93
86	MED5	DNA9A-DNA44-DNA26-DNA45-DNA37	94
87	MED6	DNA9A-DNA44-DNA26-DNA45-DNA37-DNA27	95
88	MED7	DNA9A-DNA44-DNA26-DNA45-DNA37-DNA27-DNA29	96
89	MED8	DNA9A-DNA44-DNA26-DNA45-DNA37-DNA27-DNA29-DNA5	97

SEQ ID NO: 1-116 are set out in the attached Sequence Listing. The codes for nucleotide sequences used in the attached Sequence Listing, including the symbol "n," conform to WIPO Standard ST.25 (1998), Appendix 2, Table 1.

All references cited herein, including patent references and non-patent publications, are hereby incorporated by reference in their entireties.

Although the present invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, changes and modifications can be carried out without departing from the scope of the invention which is intended to be limited only by the scope of the appended claims.